Gromiha Michael

List of Publications by Year
in descending order

258 papers	9,381 citations	53939 47 h-index	64407 83 g-index
262 all docs	262 docs citations	262 times ranked	9674 citing authors

#	Article	IF	Citations
1	Alz-Disc: A Tool to Discriminate Disease-causing and Neutral Mutations in Alzheimer's Disease. Combinatorial Chemistry and High Throughput Screening, 2023, 26, 769-777.	0.6	3
2	ProNAB: database for binding affinities of proteinâ€“nucleic acid complexes and their mutants. Nucleic Acids Research, 2022, 50, D1528-D1534.	6.5	20
3	Myxobacterial depsipeptide chondramides interrupt SARS-CoV-2 entry by targeting its broad, cell tropic spike protein. Journal of Biomolecular Structure and Dynamics, 2022, 40, 12209-12220.	2.0	10
4	Effect of charged mutation on aggregation of a pentapeptide: Insights from molecular dynamics simulations. Proteins: Structure, Function and Bioinformatics, 2022, 90, 405-417.	1.5	2
5	Elucidating important structural features for the binding affinity of spike â€•<scp>SARSâ€CoV</scp>â€2 neutralizing antibody complexes. Proteins: Structure, Function and Bioinformatics, 2022, 90, 824-834.	1.5	16
6	Srinivasan (1962â€“2021) in Bioinformatics and beyond. Bioinformatics, 2022, 38, 2377-2379.	1.8	2
7	Tumor Heterogeneity and Molecular Characteristics of Glioblastoma Revealed by Single-Cell RNA-Seq Data Analysis. Genes, 2022, 13, 428.	1.0	2
8	Understanding the mutational frequency in SARS-CoV-2 proteome using structural features. Computers in Biology and Medicine, 2022, 147, 105708.	3.9	6
9	Ab-CoV: a curated database for binding affinity and neutralization profiles of coronavirus-related antibodies. Bioinformatics, 2022, 38, 4051-4052.	1.8	1
10	Prediction of proteinâ€“carbohydrate complex binding affinity using structural features. Briefings in Bioinformatics, 2021, 22, .	3.2	9
11	Computational studies of drug repurposing and synergism of lopinavir, oseltamivir and ritonavir binding with SARS-CoV-2 protease against COVID-19. Journal of Biomolecular Structure and Dynamics, 2021, 39, 2673-2678.	2.0	325
12	MPTherm: database for membrane protein thermodynamics for understanding folding and stability. Briefings in Bioinformatics, 2021, 22, 2119-2125.	3.2	18
13	Mutations in transmembrane proteins: diseases, evolutionary insights, prediction and comparison with globular proteins. Briefings in Bioinformatics, 2021, 22, .	3.2	17
14	Why are <scp>ACE2</scp> binding coronavirus strains <scp>SARSâ€CoV</scp>/<scp>SARSâ€CoV</scp>â€2 wild and <scp>NL63</scp> mild?. Proteins: Structure, Function and Bioinformatics, 2021, 89, 389-398.	1.5	25
15	ANuPP: A Versatile Tool to Predict Aggregation Nucleating Regions in Peptides and Proteins. Journal of Molecular Biology, 2021, 433, 166707.	2.0	23
16	Predicting potential residues associated with lung cancer using deep neural network. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2021, 822, 111737.	0.4	6
17	ProThermDB: thermodynamic database for proteins and mutants revisited after 15 years. Nucleic Acids Research, 2021, 49, D420-D424.	6.5	102
18	MPTherm-pred: Analysis and Prediction of Thermal Stability Changes upon Mutations in Transmembrane Proteins. Journal of Molecular Biology, 2021, 433, 166646.	2.0	10

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19	COVID-19 outbreak: history, mechanism, transmission, structural studies and therapeutics. Infection, 2021, 49, 199-213.	2.3	160
20	Molecular dynamics simulations of cognate and non-cognate AspRS-tRNA^{Asp} complexes. Journal of Biomolecular Structure and Dynamics, 2021, 39, 493-501.	2.0	2
21	Deciphering the Role of Residues Involved in Disorder-To-Order Transition Regions in Archaeal tRNA Methyltransferase 5. Genes, 2021, 12, 399.	1.0	0
22	Understanding disorder-to-order transitions in proteinâ€“RNA complexes using molecular dynamics simulations. Journal of Biomolecular Structure and Dynamics, 2021, , 1-11.	2.0	3
23	Exploring Common Therapeutic Targets for Neurodegenerative Disorders Using Transcriptome Study. Frontiers in Genetics, 2021, 12, 639160.	1.1	11
24	Tackling Covidâ€19 using disorderedâ€toâ€order transition of residues in the spike protein upon angiotensinâ€converting enzyme 2 binding. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1158-1166.	1.5	9
25	Exploring antibody repurposing for COVID-19: beyond presumed roles of therapeutic antibodies. Scientific Reports, 2021, 11, 10220.	1.6	12
26	Evaluation of in silico tools for the prediction of protein and peptide aggregation on diverse datasets. Briefings in Bioinformatics, 2021, 22, .	3.2	5
27	Investigations on the binding specificity of Î²-galactoside analogues with human galectin-1 using molecular dynamics simulations. Journal of Biomolecular Structure and Dynamics, 2021, , 1-12.	2.0	0
28	Exploring the sequence features determining amyloidosis in human antibody light chains. Scientific Reports, 2021, 11, 13785.	1.6	16
29	PPAR-Responsive Elements Enriched with Alu Repeats May Contribute to Distinctive PPARÎ³â€“DNMT1 Interactions in the Genome. Cancers, 2021, 13, 3993.	1.7	2
30	AbsoluRATE: An in-silico method to predict the aggregation kinetics of native proteins. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140682.	1.1	8
31	Protein aggregation: in silico algorithms and applications. Biophysical Reviews, 2021, 13, 71-89.	1.5	36
32	Identification of Transcription Factors, Biological Pathways, and Diseases as Mediated by N6-methyladenosine Using Tensor Decomposition-Based Unsupervised Feature Extraction. Applied Sciences (Switzerland), 2021, 11, 213.	1.3	2
33	Guest Editorial for Special Section on the 15th International Conference on Intelligent Computing (ICIC). IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1730-1732.	1.9	0
34	Illustrative Tutorials for ProThermDB: Thermodynamic Database for Proteins and Mutants. Current Protocols, 2021, 1, e306.	1.3	0
35	A novel hybrid SEIQR model incorporating the effect of quarantine and lockdown regulations for COVID-19. Scientific Reports, 2021, 11, 24073.	1.6	11
36	AggreRATE-Pred: a mathematical model for the prediction of change in aggregation rate upon point mutation. Bioinformatics, 2020, 36, 1439-1444.	1.8	12

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37	ProAffiMuSeq: sequence-based method to predict the binding free energy change of proteinâ€“protein complexes upon mutation using functional classification. Bioinformatics, 2020, 36, 1725-1730.	1.8	28
38	Design of fluorinated sialic acid analog inhibitor to H5 hemagglutinin of H5N1 influenza virus through molecular dynamics simulation study. Journal of Biomolecular Structure and Dynamics, 2020, 38, 3504-3513.	2.0	4
39	Identifying suitable tools for variant detection and differential gene expression using RNA-seq data. Genomics, 2020, 112, 2166-2172.	1.3	8
40	Predâ€¥MutHTP: Prediction of diseaseâ€causing and neutral mutations in human transmembrane proteins. Human Mutation, 2020, 41, 581-590.	1.1	21
41	Multi-omics-based identification of SARS-CoV-2 infection biology and candidate drugs against COVID-19. Computers in Biology and Medicine, 2020, 126, 104051.	3.9	71
42	VEPAD - Predicting the effect of variants associated with Alzheimer's disease using machine learning. Computers in Biology and Medicine, 2020, 124, 103933.	3.9	14
43	New insights into the stereospecific reduction by an (S) specific carbonyl reductase fromCandida parapsilosisATCC 7330: experimental and QM/MM studies. Catalysis Science and Technology, 2020, 10, 5925-5934.	2.1	5
44	Insights into changes in binding affinity caused by disease mutations in protein-protein complexes. Computers in Biology and Medicine, 2020, 123, 103829.	3.9	21
45	ProCaff: proteinâ€“carbohydrate complex binding affinity database. Bioinformatics, 2020, 36, 3615-3617.	1.8	11
46	Role of disordered regions in transferring tyrosine to its cognate tRNA. International Journal of Biological Macromolecules, 2020, 150, 705-713.	3.6	3
47	Computational approaches for identifying potential inhibitors on targeting protein interactions in drug discovery. Advances in Protein Chemistry and Structural Biology, 2020, 121, 25-47.	1.0	9
48	CPAD 2.0: a repository of curated experimental data on aggregating proteins and peptides. Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis, 2020, 27, 128-133.	1.4	24
49	Neurodegenerative Diseases â€“ Is Metabolic Deficiency the Root Cause?. Frontiers in Neuroscience, 2020, 14, 213.	1.4	148
50	Proteinâ€“carbohydrate complexes: Binding site analysis, prediction, binding affinity and molecular dynamics simulations. , 2020, , 299-332.		4
51	Therapeutic Targets and Computational Approaches on Drug Development for COVID-19. Current Topics in Medicinal Chemistry, 2020, 20, 2210-2220.	1.0	16
52	Quantitative structureâ€“activity relationship in ligand-based drug design: Concepts and applications. , 2020, , 333-349.		0
53	Guest Editorial for Special Section on the 14th International Conference on Intelligent Computing (ICIC). IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1474-1475.	1.9	0
54	Binding affinity of proteinâ€“protein complexes: experimental techniques, databases and computational methods. , 2020, , 87-108.		1

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55	Identification of Potential Inhibitors for Targets Involved in Dengue Fever. Current Topics in Medicinal Chemistry, 2020, 20, 1742-1760.	1.0	3
56	Exploring the selective vulnerability in Alzheimer disease using tissue specific variant analysis. Genomics, 2019, 111, 936-949.	1.3	19
57	Protein Structural Bioinformatics: An Overview. , 2019, , 445-459.		23
58	Guest Editorial for Special Section on the 13th International Conference on Intelligent Computing (ICIC). IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 749-750.	1.9	0
59	Prediction of disease-associated mutations in the transmembrane regions of proteins with known 3D structure. PLoS ONE, 2019, 14, e0219452.	1.1	19
60	Investigation on the binding specificity of Agrocybe cylindracea galectin towards Î±(2,6)-linked sialyllactose by molecular modeling and molecular dynamics simulations. Journal of Carbohydrate Chemistry, 2019, 38, 566-585.	0.4	3
61	Mutational Landscape of the BAP1 Locus Reveals an Intrinsic Control to Regulate the miRNA Network and the Binding of Protein Complexes in Uveal Melanoma. Cancers, 2019, 11, 1600.	1.7	30
62	Molecular dynamics simulation studies on influenza A virus H5N1 complexed with sialic acid and fluorinated sialic acid. Journal of Biomolecular Structure and Dynamics, 2019, 37, 4813-4824.	2.0	7
63	HuVarBase: A human variant database with comprehensive information at gene and protein levels. PLoS ONE, 2019, 14, e0210475.	1.1	29
64	Structural insights into the aggregation mechanism of huntingtin exon 1 protein fragment with different polyQâ€lengths. Journal of Cellular Biochemistry, 2019, 120, 10519-10529.	1.2	14
65	Amarogentin, a secoiridoid glycoside, activates AMP- activated protein kinase (AMPK) to exert beneficial vasculo-metabolic effects. Biochimica Et Biophysica Acta - General Subjects, 2019, 1863, 1270-1282.	1.1	18
66	Seq2Feature: a comprehensive web-based feature extraction tool. Bioinformatics, 2019, 35, 4797-4799.	1.8	18
67	Statistical analysis of diseaseâ€causing and neutral mutations in human membrane proteins. Proteins: Structure, Function and Bioinformatics, 2019, 87, 452-466.	1.5	14
68	Investigating the energy crisis in Alzheimer disease using transcriptome study. Scientific Reports, 2019, 9, 18509.	1.6	23
69	Structural basis of flavonoids as dengue polymerase inhibitors: insights from QSAR and docking studies. Journal of Biomolecular Structure and Dynamics, 2019, 37, 104-115.	2.0	24
70	Forging New Scaffolds from Old: Combining Scaffold Hopping and Hierarchical Virtual Screening for Identifying Novel Bcl-2 Inhibitors. Current Topics in Medicinal Chemistry, 2019, 19, 1162-1172.	1.0	5
71	Exploring additivity effects of double mutations on the binding affinity of proteinâ€protein complexes. Proteins: Structure, Function and Bioinformatics, 2018, 86, 536-547.	1.5	7
72	MutHTP: mutations in human transmembrane proteins. Bioinformatics, 2018, 34, 2325-2326.	1.8	25

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73	Dissecting and analyzing key residues in proteinâ€DNA complexes. Journal of Molecular Recognition, 2018, 31, e2692.	1.1	7
74	Identification of type I and type II inhibitors of c-Yes kinase using in silico and experimental techniques. Journal of Biomolecular Structure and Dynamics, 2018, 36, 1566-1576.	2.0	8
75	Guest Editorial for Special Section on the 12th International Conference on Intelligent Computing (ICIC). IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1433-1435.	1.9	0
76	Identification and Analysis of Key Residues in Proteinâ€“RNA Complexes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1436-1444.	1.9	3
77	An in-silico method for identifying aggregation rate enhancer and mitigator mutations in proteins. International Journal of Biological Macromolecules, 2018, 118, 1157-1167.	3.6	20
78	Deciphering RNA-Recognition Patterns of Intrinsically Disordered Proteins. International Journal of Molecular Sciences, 2018, 19, 1595.	1.8	16
79	The non-enzymatic RAS effector RASSF7 inhibits oncogenic c-Myc function. Journal of Biological Chemistry, 2018, 293, 15691-15705.	1.6	9
80	Identification and Analysis of Key Residues Involved in Folding and Binding of Protein-carbohydrate Complexes. Protein and Peptide Letters, 2018, 25, 379-389.	0.4	7
81	Drug-Target Interactions: Prediction Methods and Applications. Current Protein and Peptide Science, 2018, 19, 537-561.	0.7	25
82	Identification of novel natural inhibitor for NorM â€“ a multidrug and toxic compound extrusion transporter â€“ an insilico molecular modeling and simulation studies. Journal of Biomolecular Structure and Dynamics, 2017, 35, 58-77.	2.0	22
83	Integrating computational methods and experimental data for understanding the recognition mechanism and binding affinity of protein-protein complexes. Progress in Biophysics and Molecular Biology, 2017, 128, 33-38.	1.4	10
84	Importance of functional groups in predicting the activity of small molecule inhibitors for Bclâ€2 and Bclâ€xL. Chemical Biology and Drug Design, 2017, 90, 308-316.	1.5	15
85	Aggregation prone regions in human proteome: Insights from largeâ€scale data analyses. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1099-1118.	1.5	25
86	PROXiMATE: a database of mutant proteinâ€“protein complex thermodynamics and kinetics. Bioinformatics, 2017, 33, 2787-2788.	1.8	56
87	Investigating mutation-specific biological activities of small molecules using quantitative structure-activity relationship for epidermal growth factor receptor in cancer. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2017, 806, 19-26.	0.4	8
88	An iterative compound screening contest method for identifying target protein inhibitors using the tyrosine-protein kinase Yes. Scientific Reports, 2017, 7, 12038.	1.6	28
89	Important amino acid residues involved in folding and binding of proteinâ€“protein complexes. International Journal of Biological Macromolecules, 2017, 94, 438-444.	3.6	16
90	Computational Approaches for Predicting Binding Partners, Interface Residues, and Binding Affinity of Proteinâ€“Protein Complexes. Methods in Molecular Biology, 2017, 1484, 237-253.	0.4	5

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91	Proteinâ€“protein interactions: scoring schemes and binding affinity. Current Opinion in Structural Biology, 2017, 44, 31-38.	2.6	103
92	Quercetin derivatives as non-nucleoside inhibitors for dengue polymerase: molecular docking, molecular dynamics simulation, and binding free energy calculation. Journal of Biomolecular Structure and Dynamics, 2017, 35, 2895-2909.	2.0	34
93	Guest Editorial for Special Section on the 11th International Conference on Intelligent Computing (ICIC). IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1104-1105.	1.9	0
94	Influence of Amino Acid Properties for Characterizing Amyloid Peptides in Human Proteome. Lecture Notes in Computer Science, 2017, , 541-548.	1.0	1
95	CPAD, Curated Protein Aggregation Database: A Repository of Manually Curated Experimental Data on Protein and Peptide Aggregation. PLoS ONE, 2016, 11, e0152949.	1.1	29
96	Organocatalytic Enantioselective Assembly of Spirooxindoleâ€naphthopyrans through Tandem Friedelâ€“Crafts Type/Hemiketalization. ChemCatChem, 2016, 8, 1708-1712.	1.8	24
97	Autoimmune Responses to Soluble Aggregates of Amyloidogenic Proteins Involved in Neurodegenerative Diseases: Overlapping Aggregation Prone and Autoimmunogenic regions. Scientific Reports, 2016, 6, 22258.	1.6	6
98	Applications of Protein Thermodynamic Database for Understanding Protein Mutant Stability and Designing Stable Mutants. Methods in Molecular Biology, 2016, 1415, 71-89.	0.4	20
99	In silico identification of essential proteins in Corynebacterium pseudotuberculosis based on protein-protein interaction networks. BMC Systems Biology, 2016, 10, 103.	3.0	24
100	PDBparam: Online Resource for Computing Structural Parameters of Proteins. Bioinformatics and Biology Insights, 2016, 10, BBI.S38423.	1.0	23
101	Prediction of change in protein unfolding rates upon point mutations in two state proteins. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 1104-1109.	1.1	3
102	Contribution of main chain and side chain atoms and their locations to the stability of thermophilic proteins. Journal of Molecular Graphics and Modelling, 2016, 64, 85-93.	1.3	25
103	Guest Editorial for Special Section on the 10th International Conference on Intelligent Computing (ICIC). IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 1-3.	1.9	2
104	The role of stabilization centers in protein thermal stability. Biochemical and Biophysical Research Communications, 2016, 471, 57-62.	1.0	9
105	Exploring preferred amino acid mutations in cancer genes: Applications to identify potential drug targets. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2016, 1862, 155-165.	1.8	28
106	Identification of dengue viral RNA-dependent RNA polymerase inhibitor using computational fragment-based approaches and molecular dynamics study. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1512-1532.	2.0	33
107	Analysis of secondary structural and physicochemical changes in proteinâ€“protein complexes. Journal of Biomolecular Structure and Dynamics, 2016, 34, 508-516.	2.0	5
108	Computational Analysis of Similar Protein-DNA Complexes from Different Organisms to Understand Organism Specific Recognition. Lecture Notes in Computer Science, 2016, , 888-894.	1.0	0

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109	Identification of potential inhibitors based on compound proposal contest: Tyrosine-protein kinase Yes as a target. Scientific Reports, 2015, 5, 17209.	1.6	33
110	Theoretical investigation on the glycan-binding specificity ofAgrocybe cylindraceagalectin using molecular modeling and molecular dynamics simulation studies. Journal of Molecular Recognition, 2015, 28, 528-538.	1.1	12
111	Development of a Machine Learning Method to Predict Membrane Protein-Ligand Binding Residues Using Basic Sequence Information. Advances in Bioinformatics, 2015, 2015, 1-7.	5.7	14
112	Analysis of protein-protein interaction networks based on binding affinity. Current Protein and Peptide Science, 2015, 17, 72-81.	0.7	10
113	Mutational studies to understand the structureâ€“function relationship in multidrug efflux transporters: Applications for distinguishing mutants with high specificity. International Journal of Biological Macromolecules, 2015, 75, 218-224.	3.6	3
114	Folding RaCe: a robust method for predicting changes in protein folding rates upon point mutations. Bioinformatics, 2015, 31, 2091-2097.	1.8	24
115	Structure based approach for understanding organism specific recognition of protein-RNA complexes. Biology Direct, 2015, 10, 8.	1.9	13
116	Identifying a potential receptor for the antibacterial peptide of sponge Axinella donnani endosymbiont. Gene, 2015, 566, 166-174.	1.0	3
117	Response to the comment on â€˜protein-protein binding affinity prediction from amino acid sequenceâ€™. Bioinformatics, 2015, 31, 978-978.	1.8	10
118	Discrimination of driver and passenger mutations in epidermal growth factor receptor in cancer. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2015, 780, 24-34.	0.4	28
119	Prediction of protein disorder on amino acid substitutions. Analytical Biochemistry, 2015, 491, 18-22.	1.1	9
120	Mammalian Mitochondrial ncRNA Database. Bioinformation, 2015, 11, 512-514.	0.2	6
121	Bioinformatics approaches for functional annotation of membrane proteins. Briefings in Bioinformatics, 2014, 15, 155-168.	3.2	42
122	GAP: towards almost 100 percent prediction for Î²-strand-mediated aggregating peptides with distinct morphologies. Bioinformatics, 2014, 30, 1983-1990.	1.8	43
123	Feature selection and classification of protein-protein complexes based on their binding affinities using machine learning approaches. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2088-2096.	1.5	32
124	Insights into the binding specificity of wild type and mutated wheat germ agglutinin towards Neu5Acî±(2â€3)Gal: a study by in silico mutations and molecular dynamics simulations. Journal of Molecular Recognition, 2014, 27, 482-492.	1.1	13
125	Proteinâ€“protein binding affinity prediction from amino acid sequence. Bioinformatics, 2014, 30, 3583-3589.	1.8	108
126	DOR â€“ a Database of Olfactory Receptors â€“ Integrated Repository for Sequence and Secondary Structural Information of Olfactory Receptors in Selected Eukaryotic Genomes. Bioinformatics and Biology Insights, 2014, 8, BBI.S14858.	1.0	19

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127	High throughput computing to improve efficiency of predicting protein stability change upon mutation. International Journal of Data Mining and Bioinformatics, 2014, 10, 206.	0.1	1
128	Prediction of RNA Binding Residues: An Extensive Analysis Based on Structure and Function to Select the Best Predictor. PLoS ONE, 2014, 9, e91140.	1.1	18
129	Distinct position-specific sequence features of hexa-peptides that form amyloid-fibrils: application to discriminate between amyloid fibril and amorphous Î²-aggregate forming peptide sequences. BMC Bioinformatics, 2013, 14, S6.	1.2	16
130	Identification of efflux proteins using efficient radial basis function networks with positionâ€specific scoring matrices and biochemical properties. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1634-1643.	1.5	11
131	Computational Approaches for Predicting the Binding Sites and Understanding the Recognition Mechanism of Proteinâ€“DNA Complexes. Advances in Protein Chemistry and Structural Biology, 2013, 91, 65-99.	1.0	25
132	Hydrophobic environment is a key factor for the stability of thermophilic proteins. Proteins: Structure, Function and Bioinformatics, 2013, 81, 715-721.	1.5	98
133	COMPUTATIONAL APPROACHES FOR UNDERSTANDING THE RECOGNITION MECHANISM OF PROTEIN COMPLEXES. , 2013, , 198-209.		0
134	Novel approach for selecting the best predictor for identifying the binding sites in DNA binding proteins. Nucleic Acids Research, 2013, 41, 7606-7614.	6.5	31
135	Role of Protein Aggregation and Interactions between Î±-Synuclein and Calbindin in Parkinsonâ€™s Disease. Lecture Notes in Computer Science, 2013, , 677-684.	1.0	0
136	Theoretical Investigation on the Binding Specificity of Sialyldisaccharides with Hemagglutinins of Influenza A Virus by Molecular Dynamics Simulations. Journal of Biological Chemistry, 2012, 287, 34547-34557.	1.6	24
137	ccPDB: compilation and creation of data sets from Protein Data Bank. Nucleic Acids Research, 2012, 40, D486-D489.	6.5	28
138	Real value prediction of protein folding rate change upon point mutation. Journal of Computer-Aided Molecular Design, 2012, 26, 339-347.	1.3	9
139	Introduction: advanced intelligent computing theories and their applications in bioinformatics. BMC Bioinformatics, 2012, 13, I1.	1.2	2
140	Relationship between amino acid properties and functional parameters in olfactory receptors and discrimination of mutants with enhanced specificity. BMC Bioinformatics, 2012, 13, S1.	1.2	7
141	Sequence Analysis and Discrimination of Amyloid and Non-amyloid Peptides. Communications in Computer and Information Science, 2012, , 447-452.	0.4	2
142	Structure-Function Relationship in Olfactory Receptors. Lecture Notes in Computer Science, 2012, , 618-623.	1.0	0
143	Machine Learning Algorithms for Predicting Protein Folding Rates and Stability of Mutant Proteins: Comparison with Statistical Methods. Current Protein and Peptide Science, 2011, 12, 490-502.	0.7	21
144	Scoring Function Based Approach for Locating Binding Sites and Understanding Recognition Mechanism of Proteinâ€™DNA Complexes. Journal of Chemical Information and Modeling, 2011, 51, 721-729.	2.5	22

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145	Sequence and structural features of binding site residues in protein-protein complexes: comparison with protein-nucleic acid complexes. Proteome Science, 2011, 9, S13.	0.7	25
146	Eukaryote-wide sequence analysis of mitochondrial Î²-barrel outer membrane proteins. BMC Genomics, 2011, 12, 79.	1.2	36
147	SVM based prediction of RNAâ€binding proteins using binding residues and evolutionary information. Journal of Molecular Recognition, 2011, 24, 303-313.	1.1	130
148	Influence of long-range contacts and surrounding residues on the transition state structures of proteins. Analytical Biochemistry, 2011, 408, 32-36.	1.1	7
149	Prediction of transporter targets using efficient RBF networks with PSSM profiles and biochemical properties. Bioinformatics, 2011, 27, 2062-2067.	1.8	74
150	Editorial [Hot topic: Protein Folding, Stability and Interactions (Guest Editor: M. Michael Gromiha)]. Current Protein and Peptide Science, 2010, 11, 497-497.	0.7	2
151	Prediction of Protein Folding Rates from Structural Topology and Complex Network Properties. IPSJ Transactions on Bioinformatics, 2010, 3, 40-53.	0.2	16
152	Dynamic and Structural Analysis of Hyperthermophilic Cold Shock Protein Stability. Kobunshi Ronbunshu, 2010, 67, 151-163.	0.2	0
153	Development of knowledge-based system for predicting the stability of proteins upon point mutations. Neurocomputing, 2010, 73, 2293-2299.	3.5	3
154	Prediction of membrane spanning segments and topology in Î²â€barrel membrane proteins at better accuracy. Journal of Computational Chemistry, 2010, 31, 217-223.	1.5	39
155	First insight into the prediction of protein folding rate change upon point mutation. Bioinformatics, 2010, 26, 2121-2127.	1.8	22
156	Understanding the Recognition Mechanism of Protein-RNA Complexes Using Energy Based Approach. Current Protein and Peptide Science, 2010, 11, 629-638.	0.7	11
157	Sequence and structural analysis of binding site residues in proteinâ€“protein complexes. International Journal of Biological Macromolecules, 2010, 46, 187-192.	3.6	14
158	Sequence and structural features of binding site residues in protein-protein complexes. , 2010, , .		0
159	Human-Readable Rule Generator for Integrating Amino Acid Sequence Information and Stability of Mutant Proteins. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 681-687.	1.9	7
160	Thermodynamic Database for Proteins: Features and Applications. Methods in Molecular Biology, 2010, 609, 97-112.	0.4	17
161	Identification and Analysis of Binding Site Residues in Protein Complexes: Energy Based Approach. Lecture Notes in Computer Science, 2010, , 626-633.	1.0	6
162	Topology Prediction of Î±-Helical and Î²-Barrel Transmembrane Proteins Using RBF Networks. Lecture Notes in Computer Science, 2010, , 642-649.	1.0	2

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163	TMFunction: database for functional residues in membrane proteins. Nucleic Acids Research, 2009, 37, D201-D204.	6.5	29
164	Revisiting â€œreverse hydrophobic effectâ€• Applicable only to coil mutations at the surface. Biopolymers, 2009, 91, 591-599.	1.2	7
165	Multiple Contact Network Is a Key Determinant to Protein Folding Rates. Journal of Chemical Information and Modeling, 2009, 49, 1130-1135.	2.5	41
166	Reliable prediction of protein thermostability change upon double mutation from amino acid sequence. Bioinformatics, 2009, 25, 2181-2187.	1.8	36
167	Energy based approach for understanding the recognition mechanism in proteinâ€“protein complexes. Molecular BioSystems, 2009, 5, 1779.	2.9	40
168	Computer Algorithms for Discriminating Protein Folds and Predicting Protein Folding Rates Based on Contact Information. , 2009, , .		0
169	Discrimination of mesophilic and thermophilic proteins using machine learning algorithms. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1274-1279.	1.5	73
170	New insight into longâ€range nonadditivity within protein doubleâ€mutant cycles. Proteins: Structure, Function and Bioinformatics, 2008, 70, 915-924.	1.5	52
171	Prediction of RNA binding sites in a protein using SVM and PSSM profile. Proteins: Structure, Function and Bioinformatics, 2008, 71, 189-194.	1.5	253
172	Thermodynamic and kinetic determinants of Thermotoga maritima cold shock protein stability: A structural and dynamic analysis. Proteins: Structure, Function and Bioinformatics, 2008, 71, 655-669.	1.5	31
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